These amendments are introduced merely to assign the correct SEQ ID NO: and to place the nucleotide sequence listing in the application, (after the specification and before the claims). It is respectfully asserted that these amendments do not add any new matter.

In view of the amendments, remarks and enclosures, the application complies with the requirements for computer readable disclosure of the biological sequences under 37 C.F.R. §1.821-1.825. This response is being submitted without a formal Notice to Comply.

If any additional fees are incurred for entry and consideration of this Amendment, the Examiner is authorized to charge any fees or credit any overpayment to Deposit Account No. 50-0320.

Respectfully submitted,
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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the specification:

Paragraph beginning at page 17, line 23 has been amended as follows:

The sequence data was then compared with amino acid sequences in searchable computer databases. Some sequences were found to be of particular interest:

a) a 10 amino acid residue sequence from he N-terminus of pernin (sequence (a) above showed only homology with an 8- base anti-thrombin protein sequence (SEQ ID NO: 9) from the terrestrial leeches (data from US patent 5,455,181 Oct 3, 1995: sequence 10).

The paragraph beginning at page 20, line 5 has been amended as follows:

A suite of non-specific primers called pUZ5 was synthesized by Gibco-BRL for the initial sequencing based on the N-terminal sequence of pernin. The general formula was

GAY GGN GAR CAR TGY AAY GAY GGN CAR AA (SEQ ID NO: 10)

Where Y represents a pyrimidine base, R represents a purine base and N represents any one of the four-nucleotide bases. Sequencing was done, initially using pUZ5 and an oligo-dT based "bottom strand" primer from PCR amplified cDNA. Sequencing was done by dye-termination cycle sequencing using "BigDye" prism technology (Applied Biosystems Incorporated, USA) according to their instructions. Products were resolved on an ABI 377 automated sequencer. Following the initial sequencing of approximately 500 base pairs pernin-specific primers were constructed and used to complete the sequencing of the pernin gene.